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CANADA/U.S. SPRUCE BUDWORMS PROGRAM -- WEST

RESEARCH REPORT

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Title: GENETIC PROFILES OF 4 WESTERN SPRUCE BUDWORM POPULATIONS

Principal Investigator: Molly Stock
Dept. of Forest Resources
University of Idaho
Moscow, Idaho 83843

208/885-6444

Thesis/
Reports
Stock,
M. W.

1. SUMMARY

Genetic profiles of western spruce budworms from 4 sites (in New Mexico, Oregon, Washington, and Montana) were obtained using electrophoresis and compared. At two sites (New Mexico and Oregon), budworms from more than one host tree species were compared. All groups exhibited very high levels of genetic similarity (.95-.99 on a scale of 0 - 1.0). Within-site, between-tree-species variation was generally less than between-site variation. Over all, Oregon budworms were most different from those at the other sites. Washington and Montana budworms were most similar to each other. Genotype distributions at the EST2 locus suggest that the Montana budworms would have a lower tolerance to the insecticide acephate (Orthene) than the other groups and that the Washington budworms might be more susceptible to carbaryl (Sevin) than other groups.

2. OBJECTIVES

The objectives of this study were to assess the genetic relationship among western spruce budworm populations which were, in 1981, the subject of CANUSA studies of WSBW population dynamics; to assess the effect of host-tree species upon differentiation among budworms at single sites; and to assess potential response of these populations to chemical control, based on genetic markers identified in previous studies.

3. METHODS

Western spruce budworm larvae were collected, in summer 1981, from a minimum of 10 trees of each species at each of 4 sites -- one each in New Mexico, Oregon, Washington, and Montana. Collections were made by

cooperating CANUSA researchers and were shipped to our laboratory at the University of Idaho with accompanying host foliage and appropriate APHIS interstate mailing permits. Insects received were from:

Los Alamos, NM -- collections from white fir, Douglas-fir, and Engelmann spruce (Wm. Waters, cooperator).

B.S. Place (Twisp??), WA -- from Douglas-fir only (Roy Beckwith, cooperator).

Union City, OR -- from grand fir and Douglas-fir (T. Torgerson, cooperator).

Missoula, MT -- from Douglas-fir only (Bob Campbell, cooperator).

Sixth instars were assayed. Those received younger were reared to the 6th stage on host foliage in the laboratory. Enzyme assays followed those described by Willhite and Stock (1982) and Castrovillo (1982) for Choristoneura spp. Genotype distributions in each collection were compared to random-mating (Hardy Weinberg) expectations. Between-collections comparisons at single loci were made using a contingency chi-square test. To assess genetic relationships over all loci, Nei's (1972) genetic identity and genetic distance values were calculated and dendrograms, based on the genetic distance values, were generated using an IMSL computer subroutine called OCLINK.

4. RESULTS

Data were obtained on 19 loci in 14 enzyme systems. These were aspartate aminotransferase (AAT, 2 loci), alcohol dehydrogenase (ADH, 1 locus), alpha-glucophosphate dehydrogenase (AGPDH, 1 locus), creatine kinase (CK, 1 locus), esterase (EST, 4 loci), isocitrate dehydrogenase (IDH, 1 locus), leucyl-aminopeptidase (LAP, 1 locus), lactate dehydrogenase

(LDH, 1 locus), malate dehydrogenase (MDH, 2 loci), malic enzyme (ME, 1 locus), phosphoglucose isomerase (PGI, 1 locus), phosphoglucomutase (PGM, 1 locus), 6-phosphoglucose dehydrogenase (6PGDH, 1 locus), and xanthine dehydrogenase (XDH, 1 locus) (Table 1). Genotype distributions at nearly all loci conformed to random-mating expectations. Exceptions were ADH (Washington and Montana), EST2 (Washington), LAP3 (Oregon/grand fir), LDH (Oregon/grand fir), MDH1 (Washington), and PGM (Washington). When single loci were compared across collections, the following observations were made: At ADH, New Mexico/white fir and Oregon/Douglas-fir budworms were most different from other groups. At EST2, Montana budworms were most different. At EST3, Washington and Montana budworms were similar to each other and quite different from other groups, having a lower frequency of the common allele (#3) and a higher frequency of allele #1. At MDH1 and PGM, Washington budworms were most different.

All groups exhibited very high levels of genetic similarity. Genetic identity values ranged from .948 (Montana/Douglas-fir vs. New Mexico/spruce) to .999 (New Mexico collections from spruce vs. white fir) (Table 2). The highest levels of similarity occurred within sites between tree species. Overall, Oregon budworms were most different from those at the other sites. Washington and Montana budworms were most similar (Figs. 1 and 2).

Genotype distributions at the EST2 locus suggest that the Montana budworms would have a lower tolerance to the insecticide acephate. While the frequency of [genotype] 3-3 individuals was about 80% or higher in all other groups at this locus, only 57% of individuals from the Montana collection were 3-3. Similarly, the frequency of 3-4 genotypes was about twice as high in the Montana group compared to the others (8% vs. 4%). EST2 data also suggested that Washington budworms might be more susceptible

to carbaryl than other groups. Washington budworms had an appreciably larger proportion of the silent allele at this locus than other groups. See Stock and Robertson (1980, 1982) for details of earlier work on this subject.

5. COOPERATION

We are most grateful to Drs. William Waters, Roy Beckwith, Torolf Torgerson, and Robert Campbell for providing us with budworm collections from New Mexico, Washington, Oregon, and Montana, respectively.

Table 1. Allele frequencies for spruce budworms from 4 geographic locations and 4 host tree species.

		Los Alamos				Twisp	Union City			Missoula
Locus	Allele	WF	DF	SP	total	DF	GF	DF	total	DF
AAT1	2	0	.02	0	.01	0	.01	.05	.02	.01
	3	1.0	.98	1.0	.99	1.0	.99	.95	.98	.98
	4	0	0	0	0	0	0	0	0	.01
	N	76	45	30	151	99	60	20	80	90
AAT2	1	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0
	N	80	45	30	155	100	80	20	100	100
ADH	2	1.0	.94	1.0	.99	.96	.98	.89	.96	.93
	3	0	.06	0	.01	.04	.02	.11	.04	.07
	N	57	26	25	108	90	58	18	76	67
AGP	1	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0
	N	80	45	30	155	100	64	20	84	100
CK	1	1.0	.99	1.0	1.0	.98	1.0	1.0	1.0	1.0
	2	0	.01	0	0	.02	0	0	0	0
	N	80	45	30	155	100	80	20	100	90
EST1	0	--	0	--	0	.01	0	0	0	.05
	1	--	.50	--	.50	.71	.85	.75	.84	.72
	2	--	.50	--	.50	.23	.15	.25	.16	.22
	3	--	0	--	0	.05	0	0	0	.01
	N	--	3	--	3	79	42	4	46	50
EST2	1	.04	.02	0	.03	0	.01	0	.01	.06
	2	.04	0	0	.02	.03	.05	0	.04	.12
	3	.85	.92	.91	.87	.86	.88	.89	.88	.71
	4	.04	.06	.06	.05	.08	.05	.05	.05	.06
	5	.04	0	.03	.03	.02	.02	.05	.02	.04
	N	69	25	17	111	100	66	19	85	47
EST3	0	0	0	0	0	.01	0	0	0	.02
	1	.02	0	0	.02	.21	.05	0	.04	.15
	2	.01	0	0	.01	.01	0	0	0	.11
	3	.95	1.0	1.0	.96	.74	.94	1.0	.94	.66
	4	.01	0	0	.01	.01	0	0	0	.05
	5	0	0	0	0	.02	.01	0	.01	0
	N	40	15	2	57	75	64	17	81	55

(continued)

Table 1. Continued.

		Los Alamos				Twisp	Union City			Missoula
Locus	Allele	WF	DF	SP	total	DF	GF	DF	total	DF
EST5	3	--	.06	--	.06	.02	--	--	--	.01
	4	--	.06	--	.06	.02	--	--	--	.03
	5	--	0	--	0	0	--	--	--	.01
	6	--	.88	--	.88	.96	--	--	--	.95
	N	--	8	--	8	22	--	--	--	49
IDH	1	1.0	1.0	1.0	1.0	.98	1.0	1.0	1.0	.99
	2	0	0	0	0	0	0	0	0	.01
	3	0	0	0	0	.01	0	0	0	0
	N	70	45	30	145	100	80	20	100	100
LAP3	1	.01	.01	.10	.02	0	.06	0	.04	0
	2	.99	.99	.90	.98	1.0	.94	1.0	.96	1.0
	N	55	34	15	104	92	34	20	54	54
LDH	0	0	0	0	0	0	.03	0	.02	.01
	1	1.0	1.0	1.0	1.0	1.0	.97	1.0	.98	.99
	N	77	41	30	148	92	74	20	94	100
MDH1	1	0	0	0	0	.03	0	0	0	0
	2	.99	1.0	.98	.99	.92	.97	1.0	.98	.98
	3	.01	0	.02	.01	.04	.03	0	.02	.02
	N	78	35	30	143	100	80	20	100	100
MDH2	1	.01	0	0	0	0	0	0	0	0
	2	.99	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0
	N	80	39	30	149	100	80	20	100	100
ME	1	.02	.03	0	.02	.01	0	0	0	0
	2	.98	.97	1.0	.98	.99	1.0	1.0	1.0	1.0
	N	80	43	30	153	100	80	20	100	100
PGI	0	0	0	0	0	0	.01	0	.01	.01
	1	.05	.06	.02	.05	.05	.03	.15	.06	.04
	2	.93	.91	.96	.93	.91	.94	.80	.91	.93
	3	.02	.02	.02	.02	.03	.01	.05	.02	.02
	4	0	.01	0	0	0	.01	0	.01	0
	N	80	45	30	155	100	77	20	97	83

(continued)

Table 1. Continued

		Los Alamos				Twisp	Union City			Missoula
Locus	Allele	WF	DF	SP	total	DF	GF	DF	total	DF
PGM	1	.18	.14	.10	.15	.19	.07	.08	.07	.13
	2	.78	.80	.88	.80	.74	.89	.83	.88	.82
	3	.03	.02	0	.02	.06	.04	.08	.05	.04
	4	.01	.03	.02	.02	0	0	0	0	0
	N	57	43	20	120	96	63	18	81	81
6PGDH	1	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0
	N	47	33	30	110	90	45	18	63	87
XDH	1	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0
	N	50	45	30	125	50	50	20	70	90

Table 2. Nei's (1972) genetic identity values. A = Collections pooled at each of 4 sites, B = budworms from different host trees at sites examined separately.

	New Mexico	Washington	Oregon	Montana
New Mexico	---			
Washington	.993	---		
Oregon	.970	.968	---	
Montana	.991	.998	.968	

A

	NM(WF)	NM(DF)	NM(SP)	WA(DF)	OR(GF)	OR(DF)	MT(DF)
NM(WF)	---						
NM(DF)	.962	---					
NM(SP)	.999	.961	---				
WA(DF)	.952	.992	.950	---			
OR(GF)	.976	.969	.977	.968	---		
OR(DF)	.978	.972	.978	.967	.997	---	
MT(DF)	.951	.990	.948	.998	.968	.965	---

B

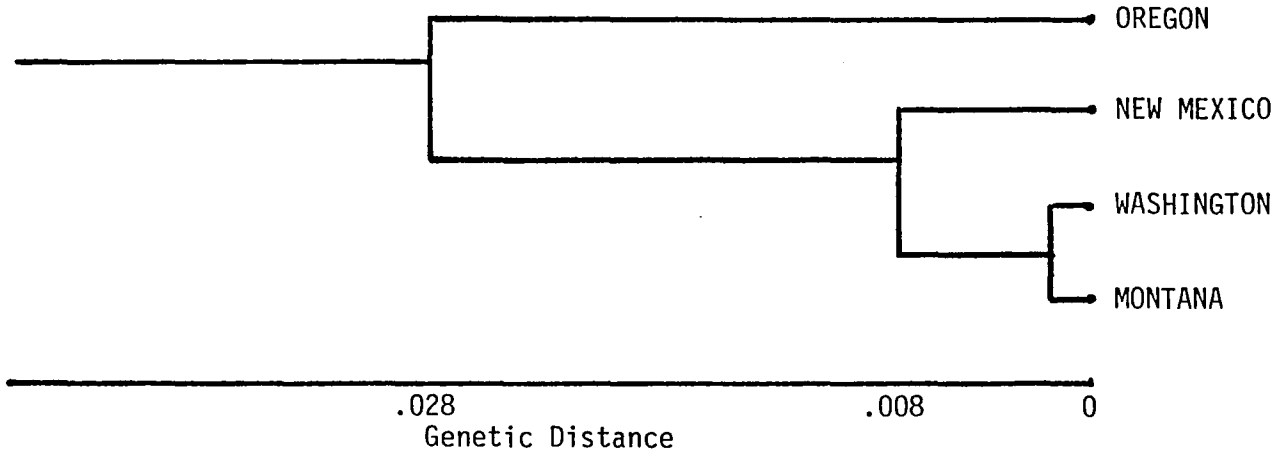

Figure 1. Genetic relationships among C. occidentalis collections from Douglas-fir at 4 sites.

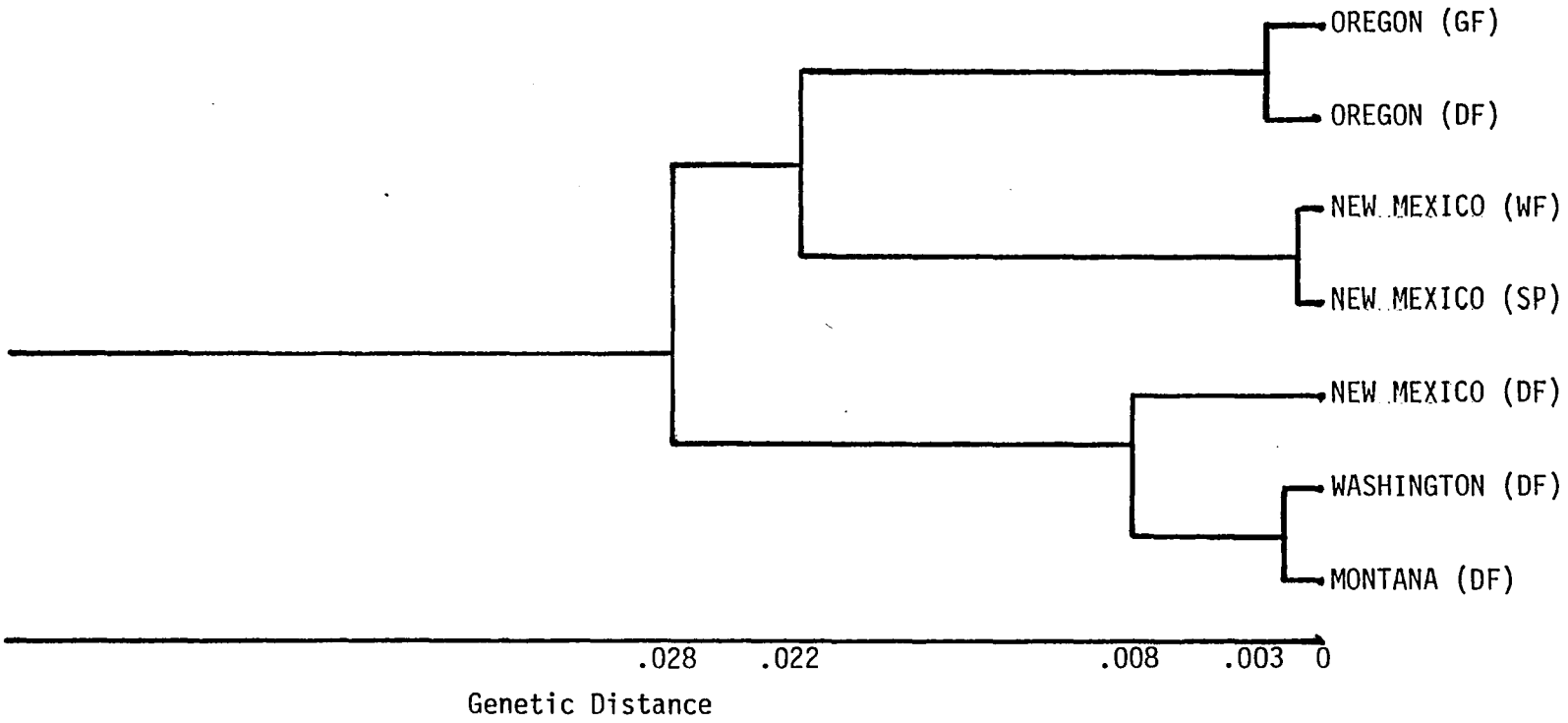

Figure 2. Genetic relationships among 7 C. occidentalis collections from 4 sites. Collections from different host tree species at a site were assayed separately. GF = grand fir, DF = Douglas-fir, WF = white fir, SP = spruce.